

#11

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/555,093

DATE: 03/01/2002  
 TIME: 15:04:43

Input Set : A:\09-555,093 sequence listing.txt  
 Output Set: N:\CRF3\03012002\I555093.raw

4 <110> APPLICANT: Napier, Johnathan A.  
 6 <120> TITLE OF INVENTION: Desaturase Genes and their Use  
 9 <130> FILE REFERENCE: 000487.00001  
 11 <140> CURRENT APPLICATION NUMBER: US 09/555,093  
 12 <141> CURRENT FILING DATE: 2000-08-22  
 14 <150> PRIOR APPLICATION NUMBER: UK 9724783.7  
 15 <151> PRIOR FILING DATE: 1997-11-24  
 17 <150> PRIOR APPLICATION NUMBER: PCT/GB98/03507  
 18 <151> PRIOR FILING DATE: 1998-11-24  
 20 <160> NUMBER OF SEQ ID NOS: 8  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1462  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: C. elegans  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (11)...(1340)  
 33 <400> SEQUENCE: 1  
 34 gctcaccaaa atg gtc gtc gac aag aat gcc tcc ggg ctt cga atg aag 49  
 35 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys 10 97  
 36 1 5  
 38 gtc gat ggc aaa tgg ctc tac ctt agc gag gaa ttg gtg aag aaa cat 10  
 39 Val Asp Gly Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His 25 145  
 40 15 20  
 42 cca gga gga gct gtt att gaa caa tat aga aat tcg gat gct act cat 45  
 43 Pro Gly Gly Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His 40 193  
 44 30 35  
 46 att ttc cac gct ttc cac gaa gga tct tct cag gct tat aag caa ctt 60  
 47 Ile Phe His Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu 55 241  
 48 50  
 50 gac ctt ctg aaa aag cac gga gag cac gat gaa ttc ctt gag aaa caa 75  
 51 Asp Leu Leu Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln 70 289  
 52 65  
 54 ttg gaa aag aga ctt gac aaa gtt gat atc aat gta tca gca tat gat 90  
 55 Leu Glu Lys Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp 85 337  
 56 80  
 58 gtc agt gtt gca caa gaa aag aaa atg gtt gaa tca ttc gaa aaa cta 105  
 59 Val Ser Val Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu 100 385  
 60 95  
 62 cga cag aag ctt cat gat gat gga tta atg aaa gca aat gaa aca tat 120  
 63 Arg Gln Lys Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr 115  
 64 110 125

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66	ttc ctg ttt aaa gcg att tca aca ctt tca att atg gca ttt gca ttt	433
67	Phe Leu Phe Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe	
68	130 135 140	
70	tat ctt cag tat ctt gga tgg tat att act tct gca tgt tta tta gca	481
71	Tyr Leu Gln Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala	
72	145 150 155	
74	ctt gca tgg caa caa ttc gga tgg tta aca cat gag ttc tgc cat caa	529
75	Leu Ala Trp Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln	
76	160 165 170	
78	cag cca aca aag aac aga cct ttg aat gat act att tct ttg ttc ttt	577
79	Gln Pro Thr Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe	
80	175 180 185	
82	ggt aat ttc tta caa gga ttt tca aga gat tgg tgg aag gac aag cat	625
83	Gly Asn Phe Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His	
84	190 195 200 205	
86	aac act cat cac gct gcc aca aat gta att gat cat gac ggt gat atc	673
87	Asn Thr His His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile	
88	210 215 220	
90	gac ttg gca cca ctt ttc gca ttt att cca gga gat ttg tgc aag tat	721
91	Asp Leu Ala Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr	
92	225 230 235	
94	aag gcc agc ttt gaa aaa gca att ctc aag att gta cca tat caa cat	769
95	Lys Ala Ser Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His	
96	240 245 250	
98	ctc tat ttc acc gca atg ctt cca atg ctc cgt ttc tca tgg act ggt	817
99	Leu Tyr Phe Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly	
100	255 260 265	
102	cag tca gtt caa tgg gta ttc aaa gag aat caa atg gag tac aag gtc	865
103	Gln Ser Val Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val	
104	270 275 280 285	
106	tat caa aga aat gca ttc tgg gag caa gca aca att gtt gga cat tgg	913
107	Tyr Gln Arg Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp	
108	290 295 300	
110	gct tgg gta ttc tat caa ttg ttc tta tta cca aca tgg cca ctt cgg	961
111	Ala Trp Val Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg	
112	305 310 315	
114	gtt gct tat ttc att att tca caa atg gga gga ggc ctt ttg att gct	1009
115	Val Ala Tyr Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala	
116	320 325 330	
118	cac gta gtc act ttc aac cat aac tct gtt gat aag tat cca gcc aat	1057
119	His Val Val Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn	
120	335 340 345	
122	tct cga att tta aac aac ttc gcc gct ctt caa att ttg acc aca cgc	1105
123	Ser Arg Ile Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg	
124	350 355 360 365	
126	aac atg act cca tct cca ttc att gat tgg ctt tgg ggt gga ctc aat	1153
127	Asn Met Thr Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn	
128	370 375 380	
130	tat cag atc gag cac cac ttg ttc cca aca atg cca cgt tgc aat ctg	1201

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131 Tyr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu
132                               385                               390                               395
134 aat gct tgc gtg aaa tat gtg aaa gaa tgg tgc aaa gag aat aat ctt      1249
135 Asn Ala Cys Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu
136                               400                               405                               410
138 cct tac ctc gtc gat gac tac ttt gac gga tat gca atg aat ttg caa      1297
139 Pro Tyr Leu Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln
140                               415                               420                               425
142 caa ttg aaa aat atg gct gag cac att caa gct aaa gct gcc t      1340
143 Gln Leu Lys Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala
144 430                               435                               440
146 aaacaatctg ggtgttcaaa aagttttttt ttgtttttta aatttaattc ttgaaatta      1400
147 ttgtttttcc gtcattcttc ctccattccc ttttctgcta gaaataaaac cttgtttttc      1460
148 aa
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 443
152 <212> TYPE: PRT
153 <213> ORGANISM: C. elegans
155 <400> SEQUENCE: 2
156 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
157 1                               5                               10                               15
158 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
159                               20                               25                               30
160 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
161                               35                               40                               45
162 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
163                               50                               55                               60
164 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
165 65                               70                               75                               80
166 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
167                               85                               90                               95
168 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
169                               100                              105                              110
170 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
171                               115                              120                              125
172 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
173                               130                              135                              140
174 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
175 145                               150                              155                              160
176 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
177                               165                              170                              175
178 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
179                               180                              185                              190
180 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
181                               195                              200                              205
182 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
183                               210                              215                              220
184 Pro Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
185 225                               230                              235                              240

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```

186 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
187                               245                               250                               255
188 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
189                               260                               265                               270
190 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
191                               275                               280                               285
192 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
193                               290                               295                               300
194 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
195 305                               310                               315                               320
196 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Ile Ala His Val Val
197                               325                               330                               335
198 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
199                               340                               345                               350
200 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
201                               355                               360                               365
202 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
203 370                               375                               380
204 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
205 385                               390                               395                               400
206 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
207                               405                               410                               415
208 Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys
209                               420                               425                               430
210 Asn Met Ala Glu His Ile Gln Ala Lys Ala Ala
211                               435                               440
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 27
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: cytochrome b5 domain
221 <221> NAME/KEY: VARIANT
222 <222> LOCATION: (1)...(27)
223 <223> OTHER INFORMATION: Xaa = Any Amino Acid
225 <400> SEQUENCE: 3
W--> 226 His Pro Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
227 1                               5                               10                               15
W--> 228 Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His
229                               20                               25
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 443
233 <212> TYPE: PRT
234 <213> ORGANISM: C. elegans
236 <400> SEQUENCE: 4
237 Met Val Val Asp Lys Asn Ala Ser Gly Leu Arg Met Lys Val Asp Gly
238 1                               5                               10                               15
239 Lys Trp Leu Tyr Leu Ser Glu Glu Leu Val Lys Lys His Pro Gly Gly
240                               20                               25                               30

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```

241 Ala Val Ile Glu Gln Tyr Arg Asn Ser Asp Ala Thr His Ile Phe His
242          35          40          45
243 Ala Phe His Glu Gly Ser Ser Gln Ala Tyr Lys Gln Leu Asp Leu Leu
244          50          55          60
245 Lys Lys His Gly Glu His Asp Glu Phe Leu Glu Lys Gln Leu Glu Lys
246 65          70          75          80
247 Arg Leu Asp Lys Val Asp Ile Asn Val Ser Ala Tyr Asp Val Ser Val
248          85          90          95
249 Ala Gln Glu Lys Lys Met Val Glu Ser Phe Glu Lys Leu Arg Gln Lys
250          100          105          110
251 Leu His Asp Asp Gly Leu Met Lys Ala Asn Glu Thr Tyr Phe Leu Phe
252          115          120          125
253 Lys Ala Ile Ser Thr Leu Ser Ile Met Ala Phe Ala Phe Tyr Leu Gln
254          130          135          140
255 Tyr Leu Gly Trp Tyr Ile Thr Ser Ala Cys Leu Leu Ala Leu Ala Trp
256 145          150          155          160
257 Gln Gln Phe Gly Trp Leu Thr His Glu Phe Cys His Gln Gln Pro Thr
258          165          170          175
259 Lys Asn Arg Pro Leu Asn Asp Thr Ile Ser Leu Phe Phe Gly Asn Phe
260          180          185          190
261 Leu Gln Gly Phe Ser Arg Asp Trp Trp Lys Asp Lys His Asn Thr His
262          195          200          205
263 His Ala Ala Thr Asn Val Ile Asp His Asp Gly Asp Ile Asp Leu Ala
264          210          215          220
265 Phe Leu Phe Ala Phe Ile Pro Gly Asp Leu Cys Lys Tyr Lys Ala Ser
266 225          230          235          240
267 Phe Glu Lys Ala Ile Leu Lys Ile Val Pro Tyr Gln His Leu Tyr Phe
268          245          250          255
269 Thr Ala Met Leu Pro Met Leu Arg Phe Ser Trp Thr Gly Gln Ser Val
270          260          265          270
271 Gln Trp Val Phe Lys Glu Asn Gln Met Glu Tyr Lys Val Tyr Gln Arg
272          275          280          285
273 Asn Ala Phe Trp Glu Gln Ala Thr Ile Val Gly His Trp Ala Trp Val
274          290          295          300
275 Phe Tyr Gln Leu Phe Leu Leu Pro Thr Trp Pro Leu Arg Val Ala Tyr
276 305          310          315          320
277 Phe Ile Ile Ser Gln Met Gly Gly Gly Leu Leu Ile Ala His Val Val
278          325          330          335
279 Thr Phe Asn His Asn Ser Val Asp Lys Tyr Pro Ala Asn Ser Arg Ile
280          340          345          350
281 Leu Asn Asn Phe Ala Ala Leu Gln Ile Leu Thr Thr Arg Asn Met Thr
282          355          360          365
283 Pro Ser Pro Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile
284          370          375          380
285 Glu His His Leu Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Ala Cys
286 385          390          395          400
287 Val Lys Tyr Val Lys Glu Trp Cys Lys Glu Asn Asn Leu Pro Tyr Leu
288          405          410          415
289 Val Asp Asp Tyr Phe Asp Gly Tyr Ala Met Asn Leu Gln Gln Leu Lys

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## VERIFICATION SUMMARY

DATE: 03/01/2002

PATENT APPLICATION: US/09/555,093

TIME: 15:04:44

Input Set : A:\09-555,093 sequence listing.txt

Output Set: N:\CRF3\03012002\I555093.raw

L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3